

Claims

1. A method of producing a plant having starch granule modification comprising introducing into a plant a nucleotide sequence comprising a limit dextrinase inhibitor gene as shown in SEQ ID No.1, a fragment thereof, or a sequence having at least 40% identity thereto.
2. A method of producing a plant according to Claim 1, wherein said starch granule modification is any one or more of an altered number of starch granules, an altered size of starch granules, an altered composition of starch granules, or an increased size uniformity of starch granules in comparison to a non-engineered plant.
3. A method of producing a plant having an altered ability to degrade starch in comparison with a non-engineered plant, the method comprising introducing into a plant a nucleotide sequence comprising a limit dextrinase inhibitor gene as shown in SEQ ID No.1, or a fragment thereof, or a sequence having at least 40% identity thereto.
4. A method according to Claim 1, 2 or 3, wherein said limit dextrinase inhibitor gene is from a plant.
5. A method according to any one of Claims 1- 4, wherein said limit dextrinase inhibitor gene has the sequence shown in any one of SEQ ID Nos. 3, 5, 7, 9, 11 or 13.
6. A method according to any one of Claims 1-4, wherein said nucleotide sequence encodes a protein comprising an amino acid sequence shown in any one of SEQ ID No.2, 4, 6, 8, 10, 12 or 14, or a fragment or variant thereof
7. A method according to any one of Claims 4-6, wherein said limit dextrinase inhibitor gene is from barley, maize, wheat or rice.
8. A method according to any one of the preceding claims, wherein said limit dextrinase inhibitor gene comprises a regulatory element involved in the control of expression of said gene.
9. A method according to Claim 8, wherein said regulatory element is a promoter which causes expression of said limit dextrinase inhibitor gene in a starch storage tissue.
10. A method according to any one of the preceding claims, wherein said limit dextrinase inhibitor gene is native to the plant into which it is introduced.
11. A method according to any one of Claims 1-9, wherein said limit dextrinase inhibitor gene is foreign to the plant into which it is introduced.
12. A method according to any one of the preceding claims, wherein expression of a gene involved in starch degradation is up-regulated.
13. A method according to any one of Claims 1-11, wherein expression of a gene involved in starch degradation is down-regulated.

14. A method according to Claim 13, wherein said expression of a gene involved in starch degradation is down-regulated by antisense down-regulation, co-suppression or double stranded RNA technology.
15. A method according to any one of Claims 11-14, wherein said gene involved in starch degradation is a starch debranching enzyme.
16. A method according to any one of Claims 11-15, wherein said gene involved in starch degradation is limit dextrinase.
17. A method according to any one of the preceding claims, wherein said plant is grown and starch is harvested from said plant.
18. A method according to Claim 17, wherein said plant is grown until fruit, seed or tubers are yielded and starch is harvested from the fruit, seed or tubers.
19. A nucleotide sequence comprising the sequence shown in SEQ ID No. 1, a fragment or complement thereof, or a sequence having at least 99% identity thereto.
20. A nucleotide sequence encoding a polypeptide comprising the amino acid sequence shown in SEQ ID No. 2, a fragment or complement thereof, or a sequence having at least 99% identity thereto.
21. A nucleotide sequence according to Claim 19 or 20, wherein said sequence is from barley.
22. A protein comprising an amino acid sequence as shown in SEQ ID No. 2, a fragment thereof, or an amino acid sequence having at least 99% identity thereto.
23. A vector comprising the nucleotide sequence of any one of Claims 19-21.
24. A vector according to Claim 23, wherein a regulatory element is operably associated with said nucleotide sequence, the regulatory element being capable of directing expression of said nucleotide sequence.
25. A vector according to Claim 23 or 24, wherein said vector is a plasmid, cosmid, virus or phage.
26. A vector according to any one of Claims 23-25, wherein said vector comprises a selectable marker gene.
27. A vector according to Claim 26, wherein said vector comprises a promoter to direct expression of said selectable marker gene in cells other than the seed.
28. A vector according to any one of Claims 23-27, wherein said vector encodes for a fusion protein comprising a limit dextrinase inhibitor protein fused to a further protein product.
29. A vector according to Claim 28, wherein said further protein product is a transit peptide or a reporter gene product.

30. A plant produced according to the method of any one of Claims 1-18.
31. A genetically-engineered plant comprising the nucleotide sequence of any one of Claims 19-21.
32. A plant comprising the vector of any one of Claims 23-29.
33. A plant according to any one of Claims 30-32, wherein said plant is maize, wheat, rice, sorghum, barley, banana, apple, tomato, pear, cassava, potato, yam, turnip, rape seed, canola, sunflower, oil palm, coconut, linseed, groundnut, soya bean or pea.
34. A plant according to any one of Claims 30-33, wherein the maximum size of starch granule is up to 50% greater than that of a non-engineered control plant.
35. A plant according to any one of Claims 30-33, wherein the maximum size of starch granule is up to 50% less than that of a non-engineered plant.
36. A plant according to any one of Claims 30-33, wherein the average size distribution of starch granules is up to 50% greater than that of a non-engineered plant.
37. A plant according to any one of Claims 30-33, wherein the average size distribution of starch granules is up to 50% less than that of a non-engineered plant.
38. A plant according to any one of Claims 30-33, wherein starch content is up to 40% greater than that of a non-engineered plant.
39. A plant according to any one of Claims 30-33, wherein starch content is up to 40% less than that of a non-engineered plant.
40. A plant according to any one of Claims 30-33, wherein the ratio of amylose to amylopectin is increased compared to that of a non-engineered plant.
41. A plant according to any one of Claim 40, wherein said ratio of amylose to amylopectin is increased by up to 50% compared to that of a non-engineered plant.
42. Propagating material of a plant produced according to the method of any one of Claims 1-18.
43. Propagating material of a plant according to Claim 42, wherein said propagating material is a seed or tuber.
44. A plant cell from a plant produced according to the method of any one of Claims 1-18.
45. A genetically-engineered plant cell comprising the nucleotide sequence of any one of Claims 19-21.
46. A plant cell comprising the vector of any one of Claims 23-29.
47. Use of a nucleotide sequence comprising a limit dextrinase inhibitor gene as shown in SEQ ID No. 1, a fragment or variant thereof, or a sequence having at least 40% identity thereto, for altering the number, size or composition of starch granules in a plant.

48. Starch obtained from the plant of any one of Claims 30-41, wherein the length of amylose chains is decreased by at least 50 glucose units in comparison to amylose from non-modified starch from a non-engineered plant.

49. Starch obtained from the plant of any one of Claims 30-41, wherein the length of amylose chains is increased by at least 50 glucose units in comparison to amylose from non-modified starch from a non-engineered plant.

50. Starch obtained from the plant of any one of Claims 30-41, wherein the ratio of amylose to amylopectin is decreased by at least 10% in comparison to starch from a non-engineered plant.

51. Starch obtained from the plant of any one of Claims 30-41, wherein the ratio of low molecular weight chains to high molecular weight chains is altered by at least 10% in comparison to starch from a non-engineered plant.

52. Starch obtained from the plant of any one of Claims 30-41, wherein the average length of low molecular weight chains of amylopectin is altered by at least 5 glucose units in comparison to starch from a non-engineered plant.

53. Starch obtained from the plant of any one of Claims 30-41, wherein the average length of high molecular weight chains of amylopectin is altered by at least 10 glucose units in comparison to starch from a non-engineered plant.

54. Starch obtained from the plant of any one of Claims 30-41, wherein the ratio of small starch granules to large granules is altered by at least 10% in comparison to starch from a non-engineered plant.